

Insect biodiversity in soft fruits - monitoring and barcoding

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Abstract

*The diversity of pest insects and beneficials as well as pollinators is being investigated in several soft fruit cultures (e.g. raspberry, blackberry, currant) in South Western Germany. The output of the project will be a database-catalogue of reference specimen for molecular and morphological identification. These barcoding data will support future studies in case that experts for morphological identification are missing, e.g. in monitoring programmes for antagonists of invasive pest such as the spotted wing drosophila *Drosophila suzukii*. During the project new and effective pest and beneficial systems could have been recorded, e.g. the blueberry aphid *Ericaphis scammelli* and its antagonist *Aphidius ericaphidis* and the citrus flatid *Metcalfa pruinosa* and its natural enemy *Neodryinus typhlocybae* which has originally been established into Italy. Also a host plant shifting of the lime seed bug *Oxycarenus lavatae* from *Malvaceae* to raspberry fruits, *Rosaceae* at least in the year 2017 has been observed in several locations in Baden-Württemberg in 2017.*

Keywords: Biodiversity, identification, beneficial insects, Barcoding of life (BOL)

Introduction

Soft fruit are a growing market. The advisory services have to face the new culture as well as pest insects and mites with their phenology that are not fully described yet. A review of relevant arthropod species in soft fruit publications had been the initial starting point (Zimmermann & Schneller 2016a). Especially searching for effective host-parasitoid-systems will help to reduce or avoid the utilization of plant protection agents. On the other hand, barcoding projects focus on larger insects groups and do not work on a cultural but more taxonomical basis (Zimmermann & Schneller 2016b).

This project will combine both: an identification tool for insects and mites in soft fruit and as well collect information on the biodiversity of species that have not been recorded in larger barcoding projects in Germany.

Material and Methods

The samples were collected with malaise traps, suction sampling, photo eclector and as well by classical methods such as cutting and incubating branches and beat sampling (Zimmermann et al. 2016, Hill et al. 2005). Sampling areas were distributed all over Baden-Württemberg in and in the area of soft fruit production. After morphological classification on a higher taxonomical level the samples had been selected especially for relevant pest and beneficial insects, e.g. parasitic hymenoptera. The identification method included morphological and molecular analysis (Zimmermann & Rumsey 2017), in many cases from the same specimen to build a reference database for future identification. Reference samples are stored in the LTZ Augustenberg insect collection.

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Results

The molecular results, e.g. new sequences will be included in existing databases such as NCBI and BOLD. Short descriptions with field record data, information on identification and antagonist systems will be provided online in a free database.

New species in this study include the blueberry aphid *Ericaphis scammelli* and its antagonist *Aphidius ericaphidis*, the citrus flatid *Metcalfa pruinosa* and its natural enemy *Neodryinus typhlocybae*, parasitic hymenoptera of psyllids such as *Psyllaephagus sp.* and records of important drosophilid parasitoids, e.g. *Pachycrepoideus vindemiae*, *Trichopria drosophilae*.

Discussion

This project had been only a first step into the “fine tuning” of larger barcoding projects that are only scratching the surface of “smaller insects”. From a practical point of view it is obvious that advisory services and farmers need more information on the arthropod biodiversity with a focus on relevant species. In the project many insect groups such as damsel bugs (*Nabis spec.*), some syrphid genera and a majority of the parasitic hymenoptera could not be identified without the help of experts on morphological characters. Some still need further sampling and including museum material to build a proper molecular reference.

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